AMENDMENTS TO THE CLAIMS

1.-147. (Canceled)

148. (Previously presented) The method of claim 1 further comprising:

preparing individual RCGs obtained from members of one or more families, determining the presence or absence of SNP alleles in the RCGs, and

comparing the RCGs of the family members by comparing the presence or absence of the SNP alleles in the RCGs of the family members.

149. (Previously presented) A method comprising:

preparing a randomly primed PCR-derived reduced complexity genome (RCG) using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,

contacting SNP-ASOs immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer and

determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a genotype.

150. (Previously presented) The method of claim 149, wherein the RCG contains less than 5% of genomic material present in a whole genome.

151. (Previously presented) The method of claim 149, wherein the RCG contains less than 1% of genomic material present in a whole genome.

152. (Previously presented) The method of claim 149, wherein the RCG contains less than 0.05% of genomic material present in a whole genome.

153. (Previously presented) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for DOP-PCR.

154. (Previously presented) The method of any one of claims 149-150, wherein the at least one PCR primer is a primer for adapter-PCR.

155. (Previously presented) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 50 nucleotide residues.

156. (Previously presented) The method of claim 149, wherein the SNP-ASOs are composed of between 10 and 25 nucleotide residues.

157. (Previously presented) A method comprising:

preparing a randomly primed PCR-derived reduced complexity genome (RCG) from a genome of a tumor cell using at least one polymerase chain reaction (PCR) primer, wherein the RCG contains less than 20% of genomic material present in a whole genome,

contacting SNP-ASOs immobilized on a surface with the RCG under hybridization conditions, wherein polymorphic loci associated with SNPs corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer, and

determining the presence or absence of a SNP allele in the RCG by hybridization of the RCG with a SNP-ASO to identify a loss of heterozygosity in the tumor.

158. (Previously presented) The method of claim 157, wherein the RCG contains less than 5% of genomic material present in a whole genome.

159. (Previously presented) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for DOP-PCR.

160. (Previously presented) The method of any one of claims 157-158, wherein the at least one PCR primer is a primer for adapter-PCR.

161. (Withdrawn) An article in one or more containers, comprising

at least one polymerase chain reaction (PCR) primer for preparing a randomly primed PCR-derived reduced complexity genome (RCG), wherein the RCG contains less than 20% of genomic material present in a whole genome, and

a set of SNP-ASOs immobilized on a surface, wherein polymorphic loci corresponding to the SNP-ASOs are present with a frequency of at least 50% in a RCG made using the at least one PCR primer,

the article designed for use with a method of any one of claims 149 and 157.

162. (Withdrawn) The article of claim 161, wherein the RCG contains less than 5% of genomic material present in a whole genome.

163. (Withdrawn) The article of any one of claims 161-162, wherein the at least one PCR primer is a primer for DOP-PCR.

164. (Withdrawn) The article of any one of claims 161-162, wherein the at least one PCR primer is a primer for adapter-PCR.

165. (Previously presented) A method for simultaneously detecting a plurality of single nucleotide polymorphism (SNP) alleles in a genomic DNA sample which comprises:

preparing a randomly-primed PCR-derived reduced complexity genome (RCG) from the genomic DNA sample;

hybridizing said RCG with an arrayed panel of oligonucleotides indicative of SNP alleles associated with said RCG; and

analyzing the hybridization pattern of said RCG with oligonucleotides to thereby determine the presence or absence of said SNP alleles.

166. (Previously presented) A method for genotyping single nucleotide polymorphism (SNP) alleles in a genomic DNA sample of a subject which comprises:

preparing a randomly-primed PCR-derived reduced complexity genome (RCG) from the genomic DNA sample;

hybridizing said RCG with an arrayed panel of SNP alleles specific for said RCG; and

analyzing the hybridization pattern of said RCG on said panel to thereby determine a genotype of said subject.